

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph starting on page 1, line 1, with the following:

This application is a continuation of U.S. Patent Application No. 09/804,690, filed March 12, 2001, which is a continuation of application Ser. No. 09/146,187, filed September 1, 1998, now U.S. Patent No. 6,248,523, which is a division of application Ser. No. 08/977,818, filed Nov. 25, 1997, now U.S. Pat. No. 5,807,995, which is a division of application Ser. No. 08/670,274, filed Jun. 13, 1996, now U.S. Pat. No. 5,891,668, which is a continuation-in-part of application Ser. No. 08/585,758, filed Jan. 16, 1996, U.S. Pat. No. 5,679,523 which claims the benefit of U.S. provisional patent application No. 60/006,856, filed Nov. 16, 1995, the disclosures of which are herein incorporated by reference.

Please replace the paragraph starting on page 6, line 3, with the following:

The full length human cDNA contains an 1140 1170 bp open reading frame, encoding a 380 390 amino acid protein (GenBank Accesion No. U82130). The human and mouse cDNAs are 86% identical at the nucleotide level. The predicted proteins are 94% identical and are distinguished by 20 amino acid mismatches and one gap. A coiled-coil domain (human TSG101 aa 231-302) and a proline-rich domain (human TSG101 aa 130-205, 32% proline) typical of the activation domains of transcription factors are highly conserved between the human and mouse proteins, with only one amino acid mismatch in each of the two domains. The leucine zipper motif in the coiled-coil domain of the human TSG101 protein is identical to the one in the mouse protein.

Please replace the paragraph starting on page 33, line 22, with the following:

A 1494 bp cloned human cDNA insert (which was deposited under the Budapest Treaty at the American Type Culture Collection, Manassas, VA 20110-2209 on June 17, 2003 with Accession No. PTA-5265) was termed full length TSG101 cDNA. Sequence analysis of this cDNA identified a 1140 bp open reading frame predicted to encode a 380 amino acid protein with a molecular mass of 42.841 kDa and a pI of 5.87. The human and mouse cDNAs are 86% identical at the nucleotide level. The predicted proteins are 94% identical and are distinguished by 20 amino acid mismatches and one gap. A coiled-coil domain (human TSG101 aa 231-302) and a proline-rich domain (human TSG101 aa 130-205, 32% proline) typical of the activation domains of transcription factors are highly conserved

between the human and mouse proteins, with only one amino acid mismatch in each of the two domains. The leucine zipper motif in the coiled-coil domain of the human TSG101 protein is identical to the one in the mouse protein. Other conserved features identified in human TSG101 include seven putative protein kinase C phosphorylation sites (aa 11, 38, 86, 89, 215, 225, 357), five potential *casein* kinase II phosphorylation sites (aa 38, 210, 249, 265, 290) and three potential N-glycosylation sites (aa 44, 150, 297). Analysis of the human TSG101 cDNA and protein sequences by the BLAST program search of NCBI database did not reveal any significant homology with the sequences for any other human genes.

Please replace the nucleic acid sequence of SEQ ID NO:3 with the following:

1 gaagggtgtg cgattgtgtg ggacggctcg gggcagccca gcagcggctg accctctgcc
61 tgcggggaaag ggagtcgcaca ggccggccgtc atggcgggtgt cggagagccca gctcaagaaa
121 atggtgtcca agtacaataa cagagaccta actgtacgtg aaactgtcaa tgtttattact
181 ctatacaaag atctcaaacc tggtttggat tcatatgttt ttaacgatgg cagttccagg
241 gaactaatga acctcaactgg aacaatccct gtgccttata gaggttaatac atacaatatt
301 ccaatatgcc tatggctact ggacacatac ccatataatc ccccttatctg ttttgtaag
361 cctacttagtt caatgactat taaaacagga aagcatgttg atgcaaatgg gaagatata
421 cttccttatac tacatgaatg gaaacaccca cagtcaagact tgttgggct tattcaggtc
481 atgattgtgg tattttggaga tgaacctcca gtcttctctc gtcctatttc ggcacccat
541 ccgcataacc aggcaacggg gccacccaaat acttcctaca tgccaggcat gccagggtga
601 atctctccat acccatccgg ataccctccc aatcccagtg gttaccagg ctgtccttac
661 ccacactgggt gtccatatacc tgccacaaca agttctcagt acccttctca gcttcctgtg
721 accactgttg gtcccaagtgg ggtatggcaca atcagcgagg acaccatccg agcctcttc
781 atctctgcccc tcagtgacaa actgagatgg cggatgaagg aggaaatggg tcgtgcccag
841 gcagagctca atgccttggaa acgaacacaaa gaagacctga aaaagggtca ccagaaaactg
901 gaagagatgg ttacccgttt agatcaagaa gttagccgagg ttgataaaaa catagaacct
961 ttgaaaaaaa aggatgaaga actcagttct gctctggaaa aaatggaaaa tcagtcgtaa
1021 aacaatgata tcgatgaagt tatcatcccc acagctccct tatacaaaca gatcctgaat
1081 ctgtatgcag aagaaaacgc tattgaagac actatcttt acttgggaga agcccttgaga
1141 agggggcgtga tagacctggaa tgtcttcgt aagcatgtac gtcttctgtc ccgtaaaacag
1201 ttccagctga gggcactaat gcaaaaaagca agaaaagactg ccggctctcag tgacccat
1261 tgacttctct gataccagct ggaggttggag ctcttctttaa agtattctt ctttccttt
1321 atcagtaggt gcccagaata agttattgca gtttatcatt caagtgtaaa atattttggaa
1381 tcaataatat attttctgtt ttcttttggg aaagactggc ttttattaaat gcactttcta
1441 tcctctgtaa actttttgtg ctgaatgttggactgtctaa ataaaatttg tttt

Please replace the amino acid sequence of SEQ ID NO:4 with the following:

MAVSESQLKKMVKYKVRDLTVRETNVITLYKDLKPVLDSYFNDGSSRELMNLGTIPVVPYRGNTY
IPICLWLDTYPNPPICFKPPTSSMTIKTGKHDANGKIYLPLYHEWKHPQSDLLGLIQVMIVVFGDEPPVFSR
PISASYPYQATGPPNTSYMPGMPGGISPYPGPPNGPSGYPGCPYPPGGPYPATSSQYPSQPPVTVGPSRDG
TISEDTIRASLISAVSDKLRWRMKEEMDRAQAELNALKTEEDLKKGHQKLEEMVTRLDQEVAEVDKNIELLKK
DEELSSALEKMENQSENNDIDEVI IPTAPLYKQILNLYAEENAIEDTIFYLGAEALRRGVIDL DVFLKHVRLLSRK
QFQLRALMOKARKTAGLSDLY